

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2003, 19:24:45 ; Search time 218 Seconds
(without alignments)
3609.437 Million cell updates/sec

Title: US-09-745-506-37

Perfect score: 1799
Sequence: 1 MDKRLALLSLINDFASLSFAE.....LEKNKIITLSETRDRPLQVY 350

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1517243 segs, 1124081882 residues
Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_plus_p2n model -DEV=yjh
-DB=/cgn2_1/USPTO_SPOOL/US09745506/runat_22082003_104403_7151/apf_query.fasta_1.519
-LOOPL=0 -LOOPEXT=0 -ONITS=bits -START=1 -END=1 -MATRIX=blsum62
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR_SCORE=pcr -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcr -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09745506.@cgn.1.1.164.@runat_22082003_104403_7151
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NRG_SCORES=0 -WAIT -DSPBLCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARR_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FEAPOP=6 -FEAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
Published Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10A_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10B_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1799	100.0	1681	14	US-10-198-846-13222 Sequence 13222, A

Result No.	Score	Query Match	Length	DB ID	Description
1	1799	100.0	1681	14	US-10-198-846-13222 Sequence 13222, A

ALIGNMENTS

RESULT 1
US-10-198-846-13222
; Sequence 13222, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Seilmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13222
; LENGTH: 1681
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

US-10-198-846-13222

Alignment Scores:

Pred. No.:	1,85e+21	Length:	168
Score:	1799.00	Matches:	350
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-745-506-37 (1-350) X US-10-198-846-13222 (1-1681)

QY	1	MetLyspLeuYsaIaLeuLeuSerSerLeuLnsApPheAlaSerLeuSerPheAlaGlu	20
Db	239	ATGATATTGAAGGCTCTCCCTTTCTTCCTTGAAATACATTTGCATCCCTCGCTTGCTGAC	298
QY	21	SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu	40
Db	299	AGTTGGGACAAATGTTGGATTACTGGTGGAAACCAAGCCACCACTACTGTTAAATACACTC	358
QY	41	PheLeuThrAsnAspLeuThrGluValMetIuGluValLeuGluInLysAlaAsp	60
Db	359	TTCTGTGACCAATGACCTGACTGACGAAGTGATGGAGGAGTGTCGCAAAAGACAGAC	418
QY	61	LeuIleLeuSerTrpHisProProGluPheArgProMetLysArgIleThrTrpAsnThr	80
Db	419	CTCATTTCTCTCTTCATCCATCCGCCCATATCTCCGACCACTGAAGGCCATATACCTGGACACA	478
QY	81	TrpLysGluArgLeuValIleArgAlaLeuGluLnsAsnArgValGlyIleTrpSerProHis	100
Db	479	TGGAGAGACGCCCTCGTGATCCGGCGCTCGAGAAACAGAGTGGGTACTACTCTTCAT	538
QY	101	ThrAlaTrpAspAlaAlaProGluGluValAsnAsnTrpLeuAlaLysGluLeuGluValA	120
Db	539	ACAGCCATATGATGCTGGCGCCCAAGGGGTCAACAACATGTTGGCTAAAGGCTTGGACCT	598
QY	121	CysThrSerArgProIleHisProSerLysAlaProAsnTrpProThrGluGluLysHis	140
Db	599	TGTACCTTCAGAGGCCATATACATCTTCCAAACCTCCCAATCACTACAGAGGAAACAC	658
QY	141	ArgValGluPheAsnValAsnTrpThrGluAspLeuLnsAspLysValMetSerAlaValLys	160
Db	659	CGAGTAGAATTCACAGTTAACTATACACCCAGAACCTGGCAAAAGCATGTCTGCAGTGAA	718
QY	161	GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr	180
Db	719	GGAAATTGACGGTGTTCCTGTCTACTTCTTTCTCTGAGACTGGTAATGAGAACAAACA	778
QY	181	ArgIleLnsLeuAsnAsnGlyThrGluLysAlaLeuMetGlnValValAspPheLeuSerArg	200
Db	779	CGGATTAATTCGAATTGTACTCAAAAGGCTTGTATGCAAGGTGATGATTTCTTCCCGG	838
QY	201	AsnLysGluLeuTrpGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLnsHis	220
Db	839	AACAACAACCTTTATCAGAAAGCGAATTTCTGTACATCGAGAAAGCCTTTCCTCTACAT	898
QY	221	ThrGlyMetGlyArgLeuGlySerThrLeuAspGluSerValSerLeuAlaThrMetLeasp	240
Db	899	ACTGGAAATGGGACCGTTATGCACACTGGATGAATCTGTCTCCGGAACCATATGAT	958
QY	241	ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGluValGlyArgThr	260
Db	959	CGAATTAATAAACAACCTTAACAACTATCTCAATTCGCTTAAGCCTTGGGTTGGGAGAACC	1018
QY	261	LeuGluSerGlnValLysValAlaValAlaLeuGlyAsnLysArgLysGlySerSerValLeuGln	280
Db	1019	TTAGAGTCTCAAGTCAAAAGTCGTGGCCCTGTCGTCTGTCTGGAGAGACGCTTCGCAG	1078
QY	281	GlyValGluAlaAspLeuTrpLeuThrGlyGluMetSerHisHisAspThrLeuAspAla	300
Db	1079	GGTTTGGAGGCTGACCTTACCTCAAGGTAGATGTCCCATCTCATGATACCTTGGATGCT	1138

QY	301	AlaSerGlnGylIleAsnValIleIleuCysGluHisSerAsnThrGluuArgGlyPheLeu	320
Db	1139	GCTTCCCAAGAAATAATGTCATCTCTGTGAACACAGCAACACTGAAAGGGGCTTCTT	1198
QY	321	SerAspLeuArgAspMetIleuAspSerHisIleuGluAsnLysIleAsnIleIleLeuSer	340
Db	1199	TCCTGACCTTCGAGATGCTGGATCTTCACACTGGAGAAATAGATTAATATCTCTATCA	1258
QY	341	GluThrAspArgAspProLeuGlnValVal	350
Db	1259	GAGACTACACAGGAGCCTCTTCAGAGTGATA	1288

RESULT 2

```

US-10-177-900-10/c
: Sequence 10, Application US/10177900
: Publication No. US20030068787A1
: GENERAL INFORMATION:
: APPLICANT: Jackson, Jennifer L.
: APPLICANT: Corley, Neil C.
: APPLICANT: Guegler, Karl J.
: APPLICANT: Arvizu, Chandra
: TITLE OF INVENTION: AN ANTIBODY SPECIFICALLY BINDING CYCLOPHILIN-TYPE PEPTIDYL-PRO
: FILE REFERENCE: PF-0582-2 CIP
: CURRENT APPLICATION NUMBER: US/10/177, 900
: CURRENT FILING DATE: 2002-06-20
: PRIOR APPLICATION NUMBER: 09/440, 828
: PRIOR FILING DATE: 1999-11-15
: PRIOR APPLICATION NUMBER: 09/136, 442
: PRIOR FILING DATE: 1998-08-19
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PERL Program
: SEQ ID NO 10
: LENGTH: 2922
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: misc-feature
: OTHER INFORMATION: Incyte ID No. US20030068787A1 023075_Mm.3
US-10-177-900-10

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Alignment Scores:	
Pred. No.:	1,92e-183
Score:	1575.00
Percent Similarity:	93.14%
Best Local Similarity:	86.29%
Query Match:	87.35%
DB:	14
	Gaps: 0

US-09-745-506-37 (1-350) x US-10-177-900-10 (1-2922)

QY	1	MetaspLeuNYSAlaleuLeuSerSerLeuAsnspPheAlaSerLeuSerPheAlaGlu	20
Db	1251	ATGATATCGAAGGCTCTTCTCTGCTGATACATTGATCCCTCTCATTTGGCGAG	1192
QY	21	SerTrpAspAsnValGlyLeuLeuValGluProSerProPheIsthrValAsnThrLeu	40
Db	1191	AGCTGGGACATGTGGGATTACTGATGGAGCCAAACCCCATCTGTAATAATCACTC	1132
QY	41	PheLeuThrAsnAspLeuThrGluValMetGluGluValLeuGluNlyValAlaAsp	60
Db	1131	TTCTGTGACCAATGACCTGACGAGAGGTCATGGACGCGGCTGTGCATAAAGGCACAC	1072
QY	61	LeuIleLeuSerTYrHisProPheIlePheArgProMetIlySarGlyIleThrTrpAsnThr	80
Db	1071	TTCATCTCTCTCAACATCCACTATTTCGCGCCCATGAAGCACATTACTGGAAAACC	1012
QY	81	TrpIlySGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTYrSerProHis	100
Db	1011	TGGAAAGGAGTCTTCGCGATCCGGGCTCTGGAGACAGATGCGCTGTACTCTCCCCAC	952
QY	101	ThrIleATrAspAlaAlaProGluGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla	120


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RESULT 4
US-10-027-632-161386/c
; Sequence 161386, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161386
; LENGTH: 817
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-161386
```

```
Alignment Scores:
Pred. No.: 1.87e-75 Length: 817
Score: 692.50 Matches: 175
Percent Similarity: 73.99% Conservative: 27
Best Local Similarity: 64.10% Mismatches: 60
Query Match: 38.49% Indels: 16
DB: 13 Gaps: 1
```

US-09-745-506-37 (1-350) x US-10-027-632-161386 (1-817)

```
OY 16 LeuserPhealaglSerTripraspnsValgluLeuValgluProserProbroHs 35
DB 786 CTCCTATTGCTAAAGTTGTGACAAATATGAA-TTACTGGTGGAAACCAAGACATCATCAT 728
OY 36 ThrValasnThrLeuPheLeuThrAsnAspLeuThrGluGluValMetGluValIleu 55
DB 727 GCTATAAACACATC-TTCCAGACCAATGACTGACTGAGGAGGATGAGAGAGGTGCTG 669
OY 56 GluIysIysAlaAspLeuIleLeuSerTyHisProProIlePheArgProMetIysArg 75
DB 668 TA-AGGAAGGCGACCTCATCTCTCCGCAATCCACCAATTTTACAGCTATAAGGCAC 610
OY 76 IletHrTrpAsnThrTripraspnsValgluLeuValIleArgAlaLeuGluIleAsnArgValglu 95
DB 609 ATAACTTGAAACCACTGGAAAGAACTCTGTAATCCAGGCTGTGAGAACCAAGTTGGT 550
OY 96 IletYSerProHisThrAlaTyAspAlaIleArgGluValIleAsnAsnTripleuAla 115
DB 549 ATGTATTTCTCCACATAGACCTATGATGCTGCACCCAGGAGGTTCGCAACTGTTGGCT 490
OY 116 IysGluLeuGluAlaCysThrSerArgProIleHisProSerIleAlaIleProAsnIlePro 135
DB 489 AAAGGCTTGGAGCTTGGAGCTGTAGCTGATGCTCTTCGAAAGCTTCCCAATGACTCC 430
OY 136 ThrGluGluAsnHisArgValgluIlePheAsnValAsnTyHisThrGluAspLeuAspIysVal 155
DB 429 ATAGAG-----AACCC-ACCGAAGACCTGGACAAAGTTC 398
OY 156 MetSerAlaVal-IysGluIleAspIleAspIleValSerValThrSerPheSerAlaArgThrGlu 175
DB 397 ACGCTCGAGTGAAGAAAGGTTGTGAATGTTCTTGTGCTCTTGTCTCCGAGGATTCGA 338
```

```
OY 175 yAsnGluGluInThrArgIleAsnLeuAsnCysThrGluIysAlaLeuMetGluValIle 195
DB 337 TGATGAAACAAACATGACTCAGCTCAGTTATATCAGAAAGCTTGTGATGACAGTAGT 278
OY 195 lAspPheLeuSerArgAsnIysGluIleTyGluIleHisThrGluIleLeuSerLeuGluIly 215
DB 277 GCGTTTCTCTCCAGACCATATAATGACATCAAGACTGAATAATATGTA-CTGGAGAA 219
OY 215 sProLeuLeuLeuHisThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerIle 235
DB 218 GCCTTTGGTTTACATATGTAATGGATGGATGTTATGCACTATGATGATATCTCTCCCT 159
OY 235 uAlaThrMetIleAspArgIleIysArgHisLeuIysLeuSerHisIleArgLeuAlaIle 255
DB 158 GACAGCATGACTGAGTAATATCAACAGCCACTTAAACTATTACATATGCTTACTAGTCT 99
OY 255 uGlyValGluArgThrLeuGlu-SerGluIysValValAlaLeuCysAlaGlySerG 275
DB 98 TAGAGTACGAGGACTGAAAGGTCTTAAGTCAAAAGTCTGGCCCTGTGTCTGTCTG 39
OY 275 lYserSerValLeuGluIleGluValGluAlaAspLeu 286
DB 38 GGAGAGGCTTCTGAGAGTATAGAGCTGACCTT 4
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RESULT 5
US-10-027-632-161387/c
; Sequence 161387, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161387
; LENGTH: 817
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-161387
```

```
Alignment Scores:
Pred. No.: 1.87e-75 Length: 817
Score: 692.50 Matches: 175
Percent Similarity: 73.99% Conservative: 27
Best Local Similarity: 64.10% Mismatches: 60
Query Match: 38.49% Indels: 16
DB: 13 Gaps: 1
```

US-09-745-506-37 (1-350) x US-10-027-632-161387 (1-817)

```
OY 16 LeuserPhealaglSerTripraspnsValgluLeuValgluProserProbroHs 35
DB 786 CTCCTATTGCTAAAGTTGTGACAAATATGAA-TTACTGGTGGAAACCAAGACATCATCAT 728
OY 36 ThrValasnThrLeuPheLeuThrAsnAspLeuThrGluGluValMetGluValIleu 55
DB 727 GCTATAAACACATC-TTCCAGACCAATGACTGACTGAGGAGGATGAGAGAGGTGCTG 669
```

Db 727 GCTAATAACATC-TTCCAGACCAATGACTGAGGAGCTGATGACGAGGTCTG 669
QY 56 GlnlyLyAlaAspLeuIleuSerTyHsProProIlePheArgPrometyArg 75
Db 668 TA-AGSAGGACGACCTCATCTCTCTGCGATCCACCAATTTTCGAGCCATTAAGGCAC 610
QY 76 IletHrTPAsnThrTrpLysGluArgValIleArgAlaLeuGluAsnArgValGly 95
Db 609 ATAACTAGAAAAACCTGGAAAGAACTCTGGTAAATCCAGGCTGTGGAAAGAAAGTGGT 550
QY 96 IletYSerProHsThrAlaTyArgAlaAlaProGlnGlyAlaAsnThrPleuAla 115
Db 549 AGTATATTTCTCCATACCTATGATGCTGACCCAGGAGACTTGGCAACTGTGTGGCT 490
QY 116 LysGlyLeuGlyAlaCysThrSerArgProIleHsProSerTyAlaProAsnTyPro 135
Db 489 AAGGGCTTGGACCTTGGACCTTGGACCTTGGACCTTGGACCTTGGACCTTGGACCTC 430
QY 136 ThrGluGlyAsnHsArgValGluPheAsnValAsnTyThrGlnAspLeuAspLysVal 155
Db 429 ATAGAG-----AACCC-ACCGAAGACCTGGACAAAGTC 398
QY 156 MetSerAlaVal-LysGlyIleAspLysValSerValThrSerPheSerAlaArgThrGly 175
Db 397 ACCTGTGACGTAAAGAGGCTGGAATGCTGTCTGCTGTCTGTCTGTCTGTCTGTCTG 338
QY 175 YAsnGluGluGlnThrArgIleAsnLeuAsnGlyThrGlnLysAlaLeuMetGlnVal 195
Db 337 TGATGAAAAACAACATGACCTGACCTGATTAATCTGACAAACCTTGTGACGAGTGT 278
QY 195 LAspPheLeuSerArgAsnLysGlnLeuTyArgGlnLysThrGlnLysLeuSerLeuTy 215
Db 277 GCTTTTCTCTCCACAGCATAAATGACATCAGAACGTAATATGTA-CTGAGAA 219
QY 215 sProLeuLeuHsThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLe 235
Db 218 GCTTTTCTCTCAATCAATGGAATGGAGTGAATGGAATGGAATGGAATGGAATGGAAT 159
QY 235 uAlaThrMetIleAspArgIleLysArgHsIleuLysLeuSerHsIleArgLeuAla 255
Db 158 GACAGCAGTACTGATTAATCAACAGCACTTAATTAATTAATTAATTAATTAATTAAT 99
QY 255 uGlyValGlyArgThrLeuGlu-SerGlnValLysValAlaLeuCysAlaGlySer 275
Db 98 TAGAGTAGCAGGAGACTGAGAGAGTTTAAAGTCAAACTCGGCCCTGTGTGTGTGT 39
QY 275 LysSerValLeuGlnGlyValGluAlaAspLeu 286
Db 38 GGAGCAGCCTCTGACAGTATAGAGCTGACCTT 4

RESULT 6
US-10-198-846-6276
; Sequence 6276, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steilmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6276
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6, 9, 16, 420, 498, 518, 520, 591, 630, 641, 643, 659, 661,
; LOCATION: 671, 674, 676, 679, 680, 681, 682, 683, 684, 685, 686, 687,
; LOCATION: 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699,
; LOCATION: 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710
; OTHER INFORMATION: n = A,T,C or G
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722,
; LOCATION: 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734,
; LOCATION: 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746,
; LOCATION: 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757
; OTHER INFORMATION: n = A,T,C or G
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769,
; LOCATION: 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781,
; LOCATION: 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793,
; LOCATION: 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804
; OTHER INFORMATION: n = A,T,C or G
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816,
; LOCATION: 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-6276
Alignment Scores:
Pred. No.: 1,03e-64 Length: 828
Score: 605.50 Matches: 123
Percent Similarity: 88.57% Conservative: 1
Best Local Similarity: 87.86% Mismatches: 11
Query Match: 33.66% Indels: 5
DB: 14 Gaps: 1

US-09-745-506-37 (1-350) x US-10-198-846-6276 (1-828)
QY 1 MetAspLeuLysAlaLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
Db 148 ATGAGATTGAGGCT 207
QY 21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHsThrValAsnThrLeu 40
Db 208 AGTTGGACAAATTTGGATTACTGCTGGAACCAAGCCACCACTACTGTAATTAACCTC 267
QY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysAlaAsp 60
Db 268 TTCCTGACCAATGACCTGACTGAGGAAGTATGAGAGAGGTGCTGCAAAAGAGCGAGAC 327
QY 61 LeuIleLeuSerTyHsProProIlePheArgPrometyArgIleHrTPAsnThr 80
Db 328 CTCATCTCTCCATCAATCCGCTATCTTCCGACCATGAGGCAATMACTGGAACACA 387
QY 81 TrpLysGluArgLeuValIleArgAlaLeuGluAsn-ArgValGlyIletYSerProH 100
Db 388 TGGAAGAGCGCTGTGTGATCCGGCTCTGGAAACAAAGAGGATCTACTCTCTCA 447
QY 100 sThrAlaTyArgAlaAlaProGlnGlyVal-AsnAsnThrPleuAlaLysGlyLeuGly 120
Db 448 TACAGCCTATGATGCTGGGCCCAAGGCGTTCAACAACCTGTTGAAANGCCTTGAG 507
QY 120 LAspThrSerArgProIleHsProSerTyAlaProAsnTyProThrGluGly 138
Db 508 CTTGTACCTTN-----GNCCTCTTAACCTAGTGATCCCGGCTGACAGA 554

RESULT 7
US-09-918-995-19746
; Sequence 19746, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

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Alignment Scores:
Pred. No.: 3,856-48 Length: 394
Score: 467.00 Matches: 90
Percent Similarity: 97.83% Conservative: 0
Best Local Similarity: 97.83% Mismatches: 2
Query Match: 25.96% Indels: 0
DB: 10 Gaps: 0

US-09-745-506-37 (1-350) x US-09-960-352-10848 (1-394)

QY 1 MetApLeuLyAlAlLeuLeuSerSerLeuSnsApPheAlaSerLeuSerPheAlaGlu 20
    |||||
Db 119 AIGGATCTCAAGGCTCTCTCTTCCCTTGATGATGACTTGGATCCCTCATTTGTCGAG 178

QY 21 SerTPAspAsnValGlyLeuLeuValGluProSerProPheOHstHnValAsnThrLeu 40
    |||||
Db 179 AGCTGGACAACATTGGATTACTGTGTGGACCGACCCACACACTGTAAACACGCTC 238

QY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnTlyAlaAsp 60
    |||||
Db 239 TTCTTACCAATGACTTGTACTAGCAAGTGAAGAGAGCGGCTGCAGAAAGCGGAT 298

QY 61 LeuLeuSerTyrHisProPheArgProMetLysArgLleThrTPAsnThr 80
    |||||
Db 299 CTCATCCTCTCCATCACCATCGGCTATTTCACCAATGAAGCGCATCCTGTGAAACA 358

QY 81 TrpLysGluArgLeuValLleArgAlaLeuGlnAsn 92
    |||||
Db 359 TGGAGAGAGCGCTGGTAAATCCGGGCACTGGAGAAC 394

RESULT 9
US-10-027-632-162668
; Sequence 162668, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 162668
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-162668

Alignment Scores:
Pred. No.: 1,1e-42 Length: 765
Score: 426.50 Matches: 103
Percent Similarity: 73.72% Conservative: 12
Best Local Similarity: 66.03% Mismatches: 31
Query Match: 23.71% Indels: 14
DB: 13 Gaps: 1

US-09-745-506-37 (1-350) x US-10-027-632-162668 (1-765)

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Db 2810 GATTATAATTATCGGAACACCCACCCATTTTCGCCGACGATTAAACACAGAT 2869
Oy 80 Thrtiplygluargheuvallleargalaleuoluasnargvalglylletyrsrpro 99
Db 2870 AATTTCAGAAAGAAATGACGCTGATTTATTAACACATATGCTGTATGCGCG 2929
Oy 100 Hsthrleatyrseralaleaproglnlyvalasnarpheualaly3glyleugly 119
Db 2930 CATACTACATGATGATTTATGACAAATGGCTAAATGATGGTTGTGATATATGGGA 2989
Oy 120 AlaCysThrSerArgProIleHisProSerLysAlaProAsnTyrProthrgluGlyAsn 139
Db 2990 ATT-----AACAGACACCACTTTTAACATAA---ACA 3019
Oy 140 HisArgValGluPheAsn-----ValAsnTyrThrclnspleuAspLysValMet 156
Db 3020 CATACGTTCCCTTAATAAAATTAAGCCGTTTGTGCGCAATTAATGACGCTCCGCAATG 3079
Oy 157 SerAlaValLysGlyLeaSpGlyVal-----SerValThrSerPhe 170
Db 3080 AGAGAGCTTTAGCTGCTACGCGCGCGGCTCAAGGTGATTTCTAAACAGATTAC 3139
Oy 171 Ser---AlaArgThrGlyAsnGluGlnThrArgIleAsnLysCysThr----- 187
Db 3140 TCTTTAATTGGAACAGAGCTTTTACACCAACACAA---GGACCAATCCACGANTGGC 3196
Oy 188 -----GlnLysAlaLeuMetGlnValValAspPheLeuSer 199
Db 3197 GAAATGTCACAGAAAGTCCGTCAGAAAGCAAAATGCAATGATTTTCCCTGAACCT 3256
Oy 200 ArgAsnLysGlnLeu-----TyrGlnLysThr----- 208
Db 3257 AAGCAGAACAAAGTCTTGACAGCTATGTACAGCGCGAATCCCTATGAGAACGGGGTAT 3316
Oy 209 GlnIleLeuSerLeuLysProLeuLeuHisThrcIymetGlyArgLysCysThr 228
Db 3317 GATGTTATACCTTAATAAATCA---TCAAAAGAAATTCGTTAGCTGCGGTGGAGTA 3373
Oy 229 LeuAspGluSerValSerLeuAlaThrMetIleAspArgIleLysArgHisLeuLysLeu 248
Db 3374 TTAGACAAAGCTGTGATTCCTTATTTTGTACACCAAGTCAAGAGCTTCCCAATG 3433
Oy 249 SerHisIleArgLeuAlaLeuGlyValGlyArgThrLeuGluSerGlnValLysValVal 268
Db 3434 GATGCTGTCGG-----KTCATTCGCAAAAGATGACTAAATGATTCACACGGGTA 3484
Oy 269 AlaLeuCysAlaGlySerGlySerSerValLeuGlnGlyVal-----GluAlaAsp 285
Db 3485 GCCATTGTGTGGAGAGGTGAAATTTCTATCATGATGATTCAGTAAACAGCGCAT 3544
Oy 286 LeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAlaAlaSerGlnGlyIle 305
Db 3545 GCTATATATACGTGATGCTATTCATACCGCACATGACATGATGCTGTAAGATTGA 3604
Oy 306 AsnValIle-----LeuCysGlnHisSerAsnThrGluArg 317
Db 3605 CCAGTTATGATCCTGCTGATTCATTGAAGCGCTTGT-----AAG 3646
Oy 318 GlyPheLeuSerAspLeuArgAspMetLeuAspSerHisLeuGluLysnLysIleAsnIle 337
Db 3647 CCARAACTGTGGAAATTAATGATCAATGAAACMAAGAAATGATGCGCGTATCCATT 3706
Oy 338 IleLeuSerGluThrAspArgAspProLeuGln 348
Db 3707 TTGATTCAGAAAGCAATACCAACCATTTTCGT 3739

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; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 2452
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-2452

Alignment Scores:
Pred. No.: 3,62e-18 Length: 1140
Score: 230.00 Matches: 89
Percent Similarity: 44.35% Conservative: 72
Best Local Similarity: 24.52% Mismatches: 154
Query Match: 12.78% Indels: 48
DB: 10 Gaps: 13

US-09-745-506-37 (1-350) x US-09-738-626-2452 (1-1140)
Oy 17 SerPheAlaGluSerTyrPAspAsnValGlyLeuLeuValGluProSerProPronHisThr 36
Db 58 GCGTGGCGGAAAGCTGGAGCAAGTGGGCTGATCTGC---GGTATCCACAGAGCTCG 114
Oy 37 ValAsnThrLeuPheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGln 56
Db 115 GTCAAGCGTCTCGATTAGCACTGATTCGATTCACCCAGCAAGCTGCGCCGCAAGCTGTGAC 174
Oy 57 LysLysAlaAspLeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIle 76
Db 175 ATGGGTTGGACATGCTGATTCATTCACACCACTTCTGCTGCTGCGGTGACGCTGTT 234
Oy 77 ThrtPAsnThrTrrPlyGluArgLeuValIleArgAlaLeuGluLysnArgValGlyIle 96
Db 235 GCTGGCGATGAGCAAAAGCAAGCTCATTCACACCTTAATTCGGCGGCGGAGTGGCACTG 294
Oy 97 TyrSerProHisThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrrPLeuAlaLys 116
Db 295 TTTTCCGCGCACACTAATTCGGGATTCGCGCGCGCCACAGTGTCAACGATTAACTCGCCGAG 354
Oy 117 GlyLeuGluLysThrSerArgProIleHisProSerLysAlaProAsnTyrProThr 136
Db 355 CTGCTGGCATCACAGCGCGCGCGCCATGCGGCACAGCGCTTTTAGCGCGCATGGACAA 414
Oy 137 GlnGlyAsnHisArgValGluPheAsnValAsnTyrThrGlnAspLeu-----AspLys 154
Db 415 TGGGCGGTGACGTTCTGCCCAAGAGTACAGCGTACCTAAAGAAAGATCTTTGCGACGCA 474
Oy 155 ValMetSerAlaValLysGly-----IleAspGlyValSer--- 166
Db 475 GGTGCGGTCGATCGCGCGCATACCGAGAGTGTGCTTTGAGATCGAAGACCGGCGCAG 534
Oy 167 -----ValThrSerPheSerAlaArgThrGlyAsnGluGlnThrArgIleAsn 183
Db 535 TTTAGCGCCCTGGAAGGGGCGAATCCGGCGAGAGGGGACGCTCGATTAG----- 582
Oy 184 LeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArgAsnLysGln 203

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RESULT 13
US-09-738-626-2452
; Sequence 2452, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI

```

Db 583 -----CTTTTAAATCCCTTGAGCTCGGACATCGAGTTTGTTCACCGCGCAACCTG 633
Qy 204 LeuTyGlnLysThrGluLeu-----SerLeuGlnLysProLeuLeu--- 218
Db 634 CGGCGCCGCGCTGACGTGGTGTGCGGAGGCTCATCCGATAGAGAGCCCTTCGAT 693
Qy 219 -----LeuHis-----ThrGlyMetGlyArgLeuGln 227
Db 694 ATTGTTGAATGACACGCGCTGAGAGTTTAGAAATGCGACCGGATTTGGTGTGGT 753
Qy 228 ThrLeuAspGlnSerValSerLeuAlaThrMetLeuAspArgIleLysArgHisLeuLys 247
Db 754 GAATTTGCGGAGCGGATGCGGCTGCGGATTTCTGTAACAAGTGGCCAAACACCTGCT 813
Qy 248 LeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr-----LeuGlnSerGlnVal 265
Db 814 GTCCACCGAA-----TGGGGCGTGGCGGCTACCGCGGATCTCTGAACAATGCTG 861
Qy 266 LysValValAlaLeuGlnValGlySerGlySerSerValLeuGlnGlyVal----- 282
Db 862 TCCCGTGTGGGCTTTCATCAGGCTCGGCTGACAGTTTCTTAACGATGATTAAGCTC 921
Qy 283 GluAlaAspLeuTyLeuThrGlyGluMetSerHisAspThrLeuAspAlaLaser 302
Db 922 GGAGTGGACGCTTTATGTCATCTGTGATCTGCGCACATCCAGTTGATGAATATCTCCGA 981
Qy 303 Gln---GlyIleAsnValIleLeuGlnSerGlnHisSerAsnThrGluArgGlyPheLeuSer 321
Db 982 GAAGTGGCGCTGACGATATGATATCTGCACACTGGCGCACGAAATTCATGAGCTTCC 1041
Qy 322 AspLeuArgAspMetLeu---AspSerHisLeuGlnLysIleAsnIleLeuSer 340
Db 1042 CAAGCCCAAGAAATTTGACAGACAAAGCCCAAGGTTGAAGTTGATGATTCGATC 1101
Qy 341 GluThrAsp 343
Db 1102 CGCACAGAC 1110

RESULT 14

US-09-738-626-1/c
: Sequence 1, Application US/09738626
: Publication No. US20020197605A1
: GENERAL INFORMATION:
: APPLICANT: NAKAGAWA, SATOSHI
: APPLICANT: MIZOGUCHI, HIROSHI
: APPLICANT: ANDO, SEIKO
: APPLICANT: HAYASHI, MIKIRO
: APPLICANT: OCHIAI, KEIKO
: APPLICANT: TOKOI, HARUHIKO
: APPLICANT: TATEISHI, NAOKO
: APPLICANT: SENOH, AKIHIRO
: APPLICANT: IKEDA, MASATO
: APPLICANT: OZAKI, AKIO
: TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
: FIDE REFERENCE: 249-125
: CURRENT APPLICATION NUMBER: US/09/738,626
: CURRENT FILING DATE: 2000-12-18
: PRIOR APPLICATION NUMBER: JP 99/377484
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: JP 00/159162
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: JP 00/280988
: PRIOR FILING DATE: 2000-08-03
: NUMBER OF SEQ ID NOS: 7059
: SOFTWARE: PatentIn ver. 3.0
: SEQ ID NO. 1
: LENGTH: 3309400
: TYPE: DNA
: ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Alignment Scores:

Pred. No.: 1,2e-12 Length: 3309400
Score: 230.00 Matches: 89
Percent Similarity: 44.35% Conservative: 72
Best Local Similarity: 24.52% Mismatches: 154
Query Match: 12.78% Indels: 48
DB: 10 Gaps: 13

US-09-745-506-37 (1-350) x US-09-738-626-1 (1-3309400)

Qy 17 SerPheAlaGlnSerThrPheAspAsnValGlyLeuLeuValGluProSerProProHisThr 36
Db 2374405 GCGTTGGCGGAAAGCTGGGCAAAAGTGGGGCTGATCTGC---GGTATCCACAGAGCTGC 2374349
Qy 37 ValAsnThrLeuPheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGln 56
Db 2374348 GTGAAGCGTGTGGGTTAGCATCTGATTCACCCAGGACAGTGGCCGACAAAGGCTGTGAC 2374289
Qy 57 LysLysAlaAspLeuIleLeuSerTyHisProProIlePheArgProMetLysArgIle 76
Db 2374288 ATGGGTTGGACATGCTGATCATTCACACCCATTCGCTGCTGGGGTGGAGCTGT 2374229
Qy 77 ThrThrAsnThrThrLysGluArgLeuValIleArgAlaLeuGlnAsnArgValGlyIle 96
Db 2374228 GCTGGGATGAGCCAAAGGACAGTATTCACACCTTAATTCGCGCGGGGTGGACACTG 2374169
Qy 97 TyrSerProHisThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnThrPheAlaLys 116
Db 2374168 TTTTCGCGGACACTAATGCGGATTCGCGGCCAGGTGTCACAGATTAACCTGCCGAG 2374109
Qy 117 GlyLeuGlyAlaCysThrSerArgProIleHisProSerLysAlaProAsnTyProThr 136
Db 2374108 CTCGTGGCATCAGCGCGCGGCGGACCCATCCGACACGCGCTTTAGCGGATGACAAA 2374049
Qy 137 GluGlyAsnHisArgValGluPheAsnValAsnTyThrGlnAspLeu-----AspLys 154
Db 2374048 TGGGGCGTGCACGTTCTGCCCAAGATGACAGCTAAGAAAGATGCTTTTCGACGA 2373989
Qy 155 ValMetSerAlaValLysGly-----IleAspGlyValSer--- 166
Db 2373988 GGTGCCGCTGCATCCGCGGACTACCGAGAGTGTGCTTTAGATGAGAAAGAACGGGCGAG 2373929
Qy 167 -----ValThrSerPheSerAlaArgThrGlnGlnGluGlnThrArgIleAsn 183
Db 2373928 TTTAGCGCGTGGAGGGGCGCAATCCGGCAGGGGCGACGTCGATAAAG----- 2373881
Qy 184 LeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArgAsnLysGln 203
Db 2373880 -----CTTTTAAATCCCTTGAGCTGGCGCATCGAGTTGTGGCACCGCGCAACCTG 2373830
Qy 204 LeuTyGlnLysThrGluIleLeu-----SerLeuGlnLysProLeuLeu--- 218
Db 2373829 CGCGCCGCGCTGCTGCTGCTGCGGAGGCTCATCCGATAGAGACCTGCTTCGAT 2373770
Qy 219 -----LeuHis-----ThrGlyMetGlyArgLeuGln 227
Db 2373769 ATTGTTGAATGACACGCGCTGAGAGTTTAGAAATGCGACCGGATTTGGTGTGGT 2373710
Qy 228 ThrLeuAspGlnSerValSerLeuAlaThrMetLeuAspArgIleLysArgHisLeuLys 247
Db 2373709 GAATTTGCGGAGCGGATGCGGCTGCGGATTTCTGTAACAAGTGGCCAAACACCTGCT 2373650
Qy 248 LeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr-----LeuGlnSerGlnVal 265
Db 2373649 GTCCACCGAA-----TGGGGCGTGGCGGCTACCGGCGGATCTCTGAACAATGCTG 2373602
Qy 266 LysValValAlaLeuGlnValGlySerGlySerSerValLeuGlnGlyVal----- 282
Db 2373601 TCCCGTGTGGGCTTTCATCAGGCTCGGCTGACAGTTTCTTAACGATGATTAAGCTC 2373542
Qy 283 GluAlaAspLeuTyLeuThrGlyGluMetSerHisAspThrLeuAspAlaLaser 302
Db 2373541 GGAGTGGACGTTATGTCATCTGTGATCTGCGCACACATCCAGTTGATGAATATCTCCGA 2373482

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